

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Yi Sun
- (B) STREET: 4841 Hillway Court
- (C) CITY: Ann Arbor
- (D) STATE: Michigan
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 48105
- (G) TELEPHONE: (313) 996-1959
- (H) TELEFAX: (313) 996-7158

(ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)

(iii) NUMBER OF SEQUENCES: 50

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..355

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 17..355

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: /note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC
Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys
1 5 10

49

GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC
Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
15 20 25

97

AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp 30 35 40	145
GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp 45 50 55	193
GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val 60 65 70 75	241
GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu 80 85 90	289
TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val 95 100 105	337
GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG Val Gln Arg Ile Gly Lys 110	385
TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTG ATCCTTGAGA GAGAGAGGAT GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTGG GAAATTCTCT ACAATTAAGA TAATTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTG TGTTTATGCT TGAGGGTTAA AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT AATCCTTTT GTGTTGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACG GTCGGGTAAA CTGTAATATG GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTGAC TTGGCCAGGA AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTT TCTGTTTTG CCGAAGGTTG TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG TTCATTATGC AATGTTTAA TAAAATATTG TGCTTGAGT TATTAAGTT TGATATATAC TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG	445 505 565 625 685 745 805 865 925 985 1045 1105 1140

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
 1 5 10 15

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..754
- (D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT				192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT				240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC				288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC				336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGAA				389
Lys				
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG				449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT				509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC				569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT				629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTGAGACTT				689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT				749
TTAAA				754

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide P1 downstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTTR

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide: P2 upstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTNNNN NNN

13

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGGATCCCC ATGGCCGACG TGAGG

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGGATCCTC ATTTGCCGAT TCTTTG

26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide P.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TATGGCTAGC ATGGCCGACG TGGAGG

26

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20	25													30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35		40												45		
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	ATG	CCT	GTC	TTA	GAT	GTC	AAG	CTG	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Met	Pro	Val	Leu	Asp	Val	Lys	Leu	
50		55														
AAA	ACA	AAC	AAG	AGG	ACT	GTG	TTG	TGG	TCT	GGG	GAG	AAT	GTA	ATC	ATT	240
Lys	Thr	Asn	Lys	Arg	Thr	Val	Leu	Trp	Ser	Gly	Glu	Asn	Val	Ile	Ile	
65		70												80		
CCT	TCC	ACA	ACT	GCT	GCA	TGT	CCC	TGT	GGG	TGAAACAGAA	CAATCGCTGC					290
Pro	Ser	Thr	Thr	Ala	Ala	Cys	Pro	Cys	Gly							
85		90														
CCTCTCTGCC	AGCAGGACTG	GGTGGTCCAA	AGAATCGGCA	AATGAGAGTG	GTTAGAAGGC											350
TTCTTAGCGC	AGTTGTTCA	AGCCCTGGTG	GATCTTGTAA	TCCAGTGC	CCC TACAAAGGCT											410
AGAACACTAC	AGGGGATGAA	TTCTCAAAT	AGGAGCCGAT	GGATCTGTGG	TCTTTGGACT											470
CATCAAAGCC	TTGGTTAGCA	TTTGTCA	TTATCTTCAG	AAATTCTCTG	TGATTAAGAA											530
GATAATTAT	TAAAGGTGGT	CCTTCCTACC	TCTGTGGTGT	GTGTCGCGCA	CACAGCTTAG											590
AAGTGCTATA	AAAAAGGAAA	GAGCTCCAAA	TTGAATCACC	TTATAATTAA	CCCATTCTA											650
TACAACAGGC	AGTGGAAAGCA	GTTCGAGAC	TTTTCGATG	CTTATGGTTG	ATCAGTTAAA											710

AAAGAATGTT ACAGTAACAA ATAAAGTGCA GTTTAAA

747

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1															
														10	15

Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
														20	25	30

Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
														35	40	45

Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Met	Pro	Val	Leu	Asp	Val	Lys	Leu	
														50	55	60

Lys	Thr	Asn	Lys	Arg	Thr	Val	Leu	Trp	Ser	Gly	Glu	Asn	Val	Ile	Ile		
														65	70	75	80

Pro	Ser	Thr	Thr	Ala	Ala	Cys	Pro	Cys	Gly						
														85	90

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..291

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC
1															15

48

TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20															30

96

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys 50 55 60	192
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 65 70 75 80	240
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 85 90 95	288
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGAA Lys	341
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT TTAAA	401 461 521 581 641 701 706

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys 50 55 60
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 65 70 75 80

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
85 90 95

Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCATCTGCA GGGTCCAG

18

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCTCAT TTGCCGATTC TTTGGAC

27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide
SAGKanMX4-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC

58

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX 4-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACCTCGGTAT GATTAAATG TTTACGGGCA ATTCATTTT ATCGATGAAT TCGAGCTCG

59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTCTCCAGTG GCAGAGAAC

19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATTAAA TGTTACGGG C

21

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48	
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His		
1	5			10						15							
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20			25									30					
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144	
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp		
35			40								45						
ACG	AGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192	
Thr	Ser	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys		
50			55								60						
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240	
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
65		70				75						80					
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288	
Asn	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn			
85			90									95					
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly		
100			105									110					
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGG											389	
LYS																	
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AAACACTACAG	GGGATGAATT	CTTCAAATAG											449	
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509	
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCCTACCTC											569	
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629	
GAATCACCTT	ATAATTAC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689	
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749	
TTAAA																754	

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20          25           30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35          40           45

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50          55           60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65          70           75           80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85          90           95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100         105          110

```

Lys

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15

```

48

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144
ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA Lys	389
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT GAATCACCTT ATAATTACCA CATTCTATA CAACAGGCAG TGGAAAGCAGT TTCGAGACTT TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT TTAAA	449 509 569 629 689 749 754

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC				336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA				389
Lys				
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG				449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT				509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC				569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT				629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT				689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT				749
TTAAA				754

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45	
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	
Lys				

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20	25													30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35		40												45		
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	AGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Ser	Leu	Arg	Cys	
50		55												60		
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Gly	Glu	Cys
65		70												80		
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85														95		
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100		105												110		
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGG											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AAACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629

GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys			
50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA AGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGAA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
AAT AAA TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC			288
Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGTT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGAA			389
Lys			
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	

Lys

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48	
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His		
1			5						10					15			
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20				25						30				
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144	
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp		
			35				40					45					
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192	
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys		
			50			55			60								
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240	
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
			65			70			75			80					
AAT	CAT	TCC	TTC	AAG	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288	
Asn	His	Ser	Phe	Lys	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
			85			90						95					
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly		
			100			105			110								
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGGA											389	
Lys																	
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449	
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTT											509	

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	

Lys

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
									25					30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
							35		40				45			
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
							50		55			60				
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Gly	Glu	Cys
					65		70			75			80			
AAT	CAT	TCC	TTC	CAC	AAC	TGC	AGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Ser	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
							85		90				95			
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GCG	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
							100		105			110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTTCAGAG	CCCTGGTGGA											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTCTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT			240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC			288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
AAT CGC AGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Ser Pro Leu Cys Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTAGAG CCCTGGTGGA			389
Lys			
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAAGTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAAGCAGT TTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	

Asn	Arg	Ser	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
100															110

Lys

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10						15	
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
20	25														30	
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35		40													45	
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50		55													60	
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
65		70													80	
AAT	AAA	TCC	TTC	AAG	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	Lys	Ser	Phe	Lys	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85															95	
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100															110	
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGGA											389
Lys																

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5			10					15							
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Gly	Gly	Asp	Lys	Met	Phe	Leu
20	25			30												
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35		40					45									
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	AGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Ser	
50		55				60										
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Gly	Glu	Cys
65		70			75				80							
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85			90					95								
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100		105				110										
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAAGAG	CCCTGGTGGAA											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

```

Lys

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT

```

144

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT				192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC AGT GTT GTG GTC TGG GGA GAA TGT				240
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys	65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC				288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC				336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA				389
Lys				
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG				449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTAGCATT TGTCAGTTTT				509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC				569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT				629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT				689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT				749
TTAAA				754

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	

Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys
 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser	
50 55 60	

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His			
1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu			
20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser			
50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	

Lys

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1	5								10					15		
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
20	25													30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT	144
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
35		40												45		
ACG	TGC	GCC	ATC	TGC	AGG	GTC	CAG	GTG	ATG	GAT	GCC	TGT	CTT	AGA	TGT	192
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	
50		55												60		
CAA	GCT	GAA	AAC	AAA	CAA	GAG	GAC	TGT	GTT	GTG	GTC	TGG	GGA	GAA	TGT	240
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Val	Trp	Gly	Glu	Cys
65		70												80		
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
85														95		
AAT	CGC	AGC	CCT	CTC	AGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Ser	Pro	Leu	Ser	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
100		105												110		
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTAGAG	CCCTGGTGGA											389
Lys																
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTACCC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

48

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG AGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp 35 40 45	144
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAAGAG CCCTGGTGGAA Lys	389
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT GAATCACCTT ATAATTTACC CATTCTATA CAACAGGCAG TGGAAGCAGT TTGAGACTT TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT TTAAA	449 509 569 629 689 749 754

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15
--

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

*Sur
at
core*